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in the claims

1. **(Amended)** A screening and/or quantification method of one or more transcriptional factors(s) present in a cell or cell lysate, said method comprising the steps of:

a. binding to an insoluble solid support double-stranded DNA sequence(s) at the concentration of at least 0.01 pmole/cm² of said solid support surface, said double-stranded DNA sequence comprising a specific sequence, said specific sequence being able to bind said one or more transcriptional factor(s)[,] and said double-stranded DNA sequence being located from the surface of the solid support by a spacer corresponding to or comprising at least a double-stranded DNA nucleotide of at least 20 base pairs;

b. putting into contact said one or more transcriptional factor(s) with said bound double-stranded DNA sequences(s)[,]; and

c. identifying and/or quantifying a signal resulting from the binding of said transcriptional factor(s) upon said double-stranded DNA sequence(s).

3. **(Amended)** The method according to claim 1, wherein the specific sequence of the double-stranded DNA sequence(s) able to bind with the transcriptional factor(s) is located at a distance of at least about 6[,]8 nm from the surface of the solid support.

5. **(Amended)** The method according to claim 1, wherein the signal resulting from the binding of the transcriptional factor upon the double-stranded DNA sequence is obtained through an enzymatic reaction.

6. **(Amended)** The method according to **[any of the preceding]claim[s] 1 [to 3]**, for the **[(possibly simultaneous)]** screening and/or quantification of multiple different transcriptional factors present in a same biological sample.

7. **(Amended)** The method according to claim 1, for the screening and/or quantification of transcriptional factors selected from the group consisting of NF-KB, AP-1, CREB, SP-1, C/EBP, GR, HIF-1, Myc, NF-AT, Oct, TBP, [and] CBF-1 and[or] factors listed in table 1.

8. (Amended) The method according to claim 1, for the screening and/or quantification of multiple different transcriptional factors upon a same support [preferably] upon the same multiwell plate.

10. (Amended) The method according to claim 1, wherein the [double-stranded DNA sequence(s) comprise(s), between the specific sequence able to bind the transcriptional factor(s) and the solid support, a]spacer between the double-stranded DNA sequence(s) and the solid support is [of]at least about 13.5 nm.

12. (Amended) The method according to claim 1, wherein the binding of the double-stranded DNA sequence(s) to the insoluble solid support is of non-covalent type and includes a binding pair comprising a first member and a second member, said first member being[are] bound to [a first member of a binding pair able to interact with a]the double-stranded DNA sequence, said second member[of said binding pair] being bound to the surface of the solid support.

34. (Amended) The method of Claim [12]36, wherein said [first member of a]binding pair is biotin/streptavidin.

New claims 36-38 have been added.